SEQUENCE LISTING

W.	>	(1) GENE	RAL II	NFORMATION:
	5	(i)	APPL:	ICANT: Chatterjee, Malaya
\ \ \		•-•		Foon, Kenneth A.
)/		•		Chatterjee, Sunil K.
	10	(ii)		E OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE REATMENT OF MELANOMA AND SMALL CELL CARCINOMA
		(iii)	NUMBI	ER OF SEQUENCES: 66
		(iv)	CORRI	ESPONDENCE ADDRESS:
•	15		(A)	ADDRESSEE: MORRISON & FOERSTER
			(B)	STREET: 755 PAGE MILL ROAD
			(C)	CITY: PALO ALTO
			(D)	STATE: CA
			(E)	COUNTRY: USA
	20		(F)	ZIP: 94304-1018
u u		(v)	COMPT	UTER READABLE FORM:
<u>l</u>			(A)	MEDIUM TYPE: Floppy disk
Ī				COMPUTER: IBM PC compatible
	25			OPERATING SYSTEM: PC-DOS/MS-DOS
Ī			(D)	SOFTWARE: PatentIn Release #1.0, Version #1.30
: ::::::::::::::::::::::::::::::::::::		(vi)	CURRI	ENT APPLICATION DATA:
ं क्राप्तकों हुनक				APPLICATION NUMBER: US
i dina	30			FILING DATE:
			(C)	CLASSIFICATION:
₫		(viii)	ATTO	RNEY/AGENT INFORMATION:
				NAME: Schiff, J. Michael
	35			REGISTRATION NUMBER: 40,253
				REFERENCE/DOCKET NUMBER: 30414-20002.21
		(ix)	TELE	COMMUNICATION INFORMATION:
		•	(A)	TELEPHONE: (415) 813-5600
	40		(B)	TELEFAX: (415) 494-0792
			(C)	TELEX: 706141
		(2) INFO	RMATI	ON FOR SEQ ID NO:1:
	45	(i)	SEQU	ENCE CHARACTERISTICS:
			(A)	LENGTH: 447 base pairs
			/p\	MVDP. muslois osid

(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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					AME/1 OCAT:			447						•			
5		/ 4) FE												٠		
3		(1X	•		e: Ame/1	KEY:	mat	pept	tide								
			(1	B) L	OCAT:	ION:	58	_				•					•
		(xi) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID No	0:1:						
10	3 ma		mma	aam			a ma			~~~							
		AAG Lys															48
	-19				-15	3				-10					-5		
15	TCC	AGC	GAT	GAT	GTT	TTC	ATG	ACC	CAA	ACT	CCA	CTC	TCC	CTG	CCT	GTC	96
		Ser															
				1				5				•	10				
	AGT	CTT	GGA	GAT	CAA	GCC	TCC	ATC	TCT	TGC	AGA	TCT	AGT	CAG	AGC	ATT	144
20	Ser	Leu	_	Asp	Gln	Ala		Ile	Ser	Cys	Arg		Ser	Gln	Ser	Ile	
		15	•				20					25					
	GTA	CAT	AGT	AAT	GGA	AAC	ACC	TAT	TTA	GAA	TGG	TAC	CTA	CAG	AAA	CCA	192
25		His	Ser	Asn	Gly		Thr	Tyr	Leu	Glu	_	Tyr	Leu	Gln	Lys		
25	30					35					40					45	
		CAG															240
	Gly	Gln	Ser	Pro		Leu	Leu	Ile	Tyr		Val	Ser	Asn	Arg			
30					50					55					60		
	GGG	GTC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGA	TCA	GGG	ACA	GAT	ŢTC	ACA	288
	Gly	Val	Pro		Arg	Phe	Ser	Gly		Gly	Ser	Gly	Thr		Phe	Thr	
				65					. 70 					75			
35	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	GAG	GAT	CTG	GGA	GTT	TAT	TAC	TGC	336
	Leu	Lys		Ser	Arg	Val	Glu		Glu	Asp	Leu	Gly	Val	Tyr	Tyr	Cys	
			80					85					90				·
	TTT	CAA	GGT	TCA	CAT	GTT	CCG	TGG	ACG	TTC	GGT	GGA	GGC	ACC	AAG	CTG	384
40	Phe	Gln	Gly	Ser	His	Val		Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	
		95	•				100					105					
	GAA	ATC	AAA	CGG	GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC	TTC	CCA	CCA	432
45		Ile	Lys	Arg	Ala	_	Ala	Ala	Pro	Thr		Ser	Ile	Phe	Pro		
45	110					115					120					125	*
	TCC	AGT	AAG	CTT	GGG												447
•	Ser	Ser	Lys	Leu	_	•											
50					130					•							
50	(2)	INF	ORMA'	TION	FOR	SEO	ID 1	NO:2	:								

(ix) FEATURE:

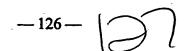
	5	(A) LENGTH: 149 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
	3	(ii) MOLECULE TYPE: protein	
•		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
	10	et Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Al 19 -15 -10 -5	.a
	15	er Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Va 1 5 10	ίl
	15	er Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Il 15 20 25	.e
	20	al His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pr 30 35 40 4	:0 15
4. 3. 4. 6. 4. 6. 6.		ly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Se 50 55 60	r
¥ N ¥	25	ly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Th	ır
	20	eu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cy 80 85 90	78
	30	he Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Le 95 100 105	:u
	35	lu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pr 10 115 120 12	
		er Ser Lys Leu Gly 130	
	40	2) INFORMATION FOR SEQ ID NO:3:	
		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 458 base pairs	
	45	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: DNA (genomic)	
	50	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1456	

(i) SEQUENCE CHARACTERISTICS:

		(ix)	(2	ATURI A) Ni B) L	AME/I		_	_pept	tide								
5		(xi)) SE	QUEN	CE DI	ESCR	IPTIC	ON: S	SEQ :	ID NO	0:3:						٠
		GCT Ala															48
10	-19				-15				•	-10					-5	•	
		CTG															96
	vaı	Leu	ser	GIn 1	Val	GIn	vai	Lys 5	GIU	ser	GTA	Pro	Phe 10	Leu	Val	Pro	
15	CCC	TCA	CAG	AGC	CTG	TCC	ATC	ACA	TGC	ACT	GTC	TCA	GGG	TTC	TCA	тта	144
		Ser 15															
20	ACC	ACC	TAT	GGT	GTA	AGC	TGG	ATT	CGC	CAG	CCT	CCA	GGA	AAG	GGT	CTG	192
	Thr	Thr				Ser					Pro					Leu	
	30					35				•	40					45	
25		TGG															240
	GIU	Trp	Leu	GIĀ	50	m	тър	GIY	Asp	55 55	THE	inr	ASI	TYL	60	ser	
	_	CTC	_												,		288
30	Ala	Leu	Ile	Ser 65	Arg	Leu	Ser	Ile	Ser 70	Lys	Asp	Asn	Ser	Lys 75	Ser	Gln	•
		TTC															336
•	Val	Phe	Leu 80	Lys	Leu	Asn	Ser	Leu 85	Gln	Thr	Asp	Asp	Thr 90	Ala	Thr	Tyr	
35																	
		TGT Cys															384
	_	95		-			100	-	_			105	-	٠, -	-		
40		ACC															432
	Gly 110	Thr	Ser	Val	Thr	Val 115	Ser	Ser	Ala	Lys	Thr 120	Thr	Pro	Pro	Pro	Val 125	
	TAT	CCA	TTG	GTC	CCT	GGA	AGC	TTG	GG		•						458
45	Tyr	Pro	Leu	Val	Pro 130	Gly	Ser	Leu									
	(2)	INF	ORMA	TION	FOR	SEQ	ID I	NO:4	:								

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(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(A) LENGTH: 152 amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5		(:	xi)	SEQU	ENCE	DES	CRIP	rion:	: SEÇ	O ID	NO:	4:				
	Met -19	Ala	Val	Leu	Gly -15	Leu	Leu	Phe	Cys	Leu -10	Val	Thr	Phe	Pro	Ser -5	Cys
10	Val	Leu	Ser	Gln 1	Val	Gln	Val	Lys 5	Glu	Ser	Gly	Pro	Phe 10	Leu	Val	Pro
15	Pro	Ser 15	Gln	Ser	Leu	Ser	Ile 20	Thr	Сув	Thr	Val	Ser 25	Gly	Phe	Ser	Leu
	Thr 30	Thr	Tyr	Gly	Val	Ser 35	Trp	Ile	Arg	Gln	Pro 40	Pro	Gly	Lys	Gly	Leu 45
20	Glu	Trp	Leu	Gly	Ala 50	Ile	Trp	Gly	Asp	Gly 55	Thr	Thr	Asn	Tyr	His 60	Ser
	Ala	Leu	Ile	Ser 65	Arg	Leu	Ser	Ile	Ser 70	Lys	Asp	Asn	Ser	Lys 75	Ser	Gln
25	Val	Phe	Leu 80	Lys	Leu	Asn	Ser	Leu 85	Gln	Thr	Asp	Asp	Thr 90	Ala	Thr	Tyr
30	Tyr	Суs 95	Ala	Lys	Leu	Gly	Asn 100	Tyr	Asp	Ala	Leu	Asp 105		Trp	Gly	Gln
	Gly 110	Thr	Ser	Val	Thr	Val 115		Ser	Ala	Lys	Thr 120	Thr	Pro	Pro	Pro	Val 125
35	Tyr	Pro	Leu	Val	Pro 130	Gly	Ser	Leu								
	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:5	:							
40		(i)	() (1 ()	A) Li B) T C) S	CE CI ENGTI YPE: I'RANI OPOLO	H: 98 amir DEDNI	3 am: 10 ac 288:	ino a cid sing	acida	3			-			·
45		(xi	SE	QUEN	CE DI	ESCR	PTI	ON: S	SEQ :	ED NO	0:5:					
		Glı	n Vai	l Glı	n Val	l Lys	Glı	ı Sei	r Gly	y Pro	o Phe	e Lei	ı Va	l Pro	o Pro	Ser Gli



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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr

		Gly	Val	Ser 35	Trp	Ile	Arg	Gln	Pro 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Leu
5		Gly	Ala 50	Ile	Trp	Gly	Asp	Gly 55	Thr	Thr	Asn	Tyr	His 60	Ser	Ala	Leu	Ile
		Ser 65	Arg	Leu	Ser	Ile	Ser 70	Lys	Asp	Asn	Ser	Lys 75	Ser	Gln	Val	Phe	Leu 80
10		Lys	Leu	Asn	Ser	Leu 85	Gln	Thr	Asp	Asp	Thr 90	Ala	Thr	Tyr	Tyr	Cys 95	Ala
15		Lys	Leu					·									
	(2)	INFO	RMATI	ON I	FOR S	SEQ 1	ID NO	0:6:									
20		(i)	(B)	JENCI LEN TYI STI	NGTH: PE: & RANDI	: 19 amino EDNES	amir aci SS: £	no ad id singl	cids								
25		(xi)	SEQU	JENCI	E DES	CRII	PTIO	1: SI	EQ II	ON C	:6:						
20		Gly 1	Asn	Tyr	Asp	Ala 5	Leu	Asp	Trp	Trp	Gly 10	Gln	Gly	Thr	Ser	Val 15	Thr
30		Val	Ser	Ser													
	(2)	INFO	RMATI	ON I	FOR S	SEQ I	ID NO): 7:									
35		(i)	(B) (C)	JENCI LEN TYI STI	NGTH: PE: 8 RANDI	: 9 a amino EDNES	amino aci	o aci ld singl	ids								
40		(xi)	SEQU	JENCI	E DE	CRI	PTIO	1: SI	EQ II) ио:	:7:						
	•	Tyr 1	Asp	Tyr	Glu	Xaa 5	Xaa	Xaa	Xaa	Xaa							
45	(2)	INFO	RMAT	ON I	FOR S	SEQ I	ID NO	9:8:									
50		(i)	(B)	UENCI LEN TYI STI	NGTH: PE: 8 RANDI	: 7 a amino EDNES	amino o ac:	o ac: id sing:	ids								

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: Xaa Xaa Xaa Xaa Xaa Xaa 5 (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids 10 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: 15 Ser Val Ser Ile Tyr Tyr Tyr Gly Arg Ser Asp Lys (2) INFORMATION FOR SEQ ID NO:10: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 25 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: Xaa Xaa Xaa Xaa Xaa 30 (2) INFORMATION FOR SEQ ID NO:11: (i) SEQUENCE CHARACTERISTICS: 35 (A) LENGTH: 4 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: Xaa Xaa Xaa Xaa 45 (2) INFORMATION FOR SEQ ID NO:12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4 amino acids (B) TYPE: amino acid 50 (C) STRANDEDNESS: single (D) TOPOLOGY: linear



	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
5	Arg Asp Tyr Arg	
	(2) INFORMATION FOR SEQ ID NO:13:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Gly Tyr Tyr Asp Xaa 1 5	
20	(2) INFORMATION FOR SEQ ID NO:14: (i) SEQUENCE CHARACTERISTICS:	-
25	(A) LENGTH: 5 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: Xaa Xaa Xaa Xaa	
30	1 5	
	(2) INFORMATION FOR SEQ ID NO:15:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
40	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
45	Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gl 1 5 10 15	y
·	Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Se 20 25 30	r
50	Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Lys Gly Gln Se 35 40 45	r

		Pro	Lys 50	Leu	Leu	Ile	Tyr	Phe 55	Val	Ser	Asn	Arg	Phe 60	Ser	Gly	Val	Pro
5	•	Asp 65	Arg	Phe	Ser	Gly	Ser 70	Gly	Ser	Gly	Thr	Asp 75	Phe	Thr	Leu	Lys	11e 80
		Ser	Arg	Val	Glu	Ala 85	Glu	Asp	Leu	Gly	Val 90	Tyr	Tyr	Сув	Phe	Gln 95	Gl
10		Ser	His	Val	Pro 100	Trp	Thr	Phe	Gly	Gly 105	Gly	Thr	Lys	Leu	Glu 110	Ile	Lys
	(2)	INFO	RMAT:	ON 1	FOR S	SEQ :	ID NO	0:16	:							•	
15		(i)	(B)	LEI TYI	NGTH: PE: & RANDI	: 119 amino EDNES	TERIS 9 am: o ac: SS: s lines	ino a id sing:	acid	3 ·							
20		(ii)	MOLI	CULI	E TYI	PE: 1	pept:	ide									
		(xi)					_		EO II	O NO	:16:						
25												T.011	V=1	Δla	Pro	Ser	G1+
23		1	Val	GIII	Leu	5	GIU	SEI	GIY	PIO	10	Deu	Val	ALG	PIO	15	
30		Ser	Leu	Ser	Ile 20	Thr	Сув	Thr	Val	Ser 25	Gly	Phe	Ser	Leu	Thr 30	Ser	Туз
		Gly	Val	His 35	Trp	Val	Arg	Gln	Pro 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Let
35		Gly	Val 50	Ile	Trp	Gly	Asp	Gly 55	Ser	Thr	Asn	Tyr	Asn 60	Ser	Ala	Leu	Lys
		Ser 65	Arg	Leu	Ser	Ile	Şer 70	Lys	Asp	Asn	Ser	Lys 75	Ser	Gln	Val	Phe	Let 80
40		Lys	Met	Asn	Ser	Leu 85	Gln	Thr	Asp	Asp	Thr 90	Ala	Arg	Tyr	Tyr	Сув 95	Ala
45		Arg	Glu	Xaa	Xaa 100		Xaa	Tyr	Tyr	Ala 105	Met	Asp	Tyr	Trp	Gly 110	Gln	Gl
		Thr	Ser	Val 115	Thr	Val	Ser	Ser		•							
50	(2)	INFO													•		
÷		(1)	SEQ (A				TERI: 6 ba:										

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	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
10	GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
10	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
15	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
20	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
20	(2) INFORMATION FOR SEQ ID NO:18:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	٠
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
	GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
35	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
40	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
45	(2) INFORMATION FOR SEQ ID NO:19:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 336 base pairs(B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single	

(B) TYPE: nucleic acid

	(II) Nombold III . DAY (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
5	GATGTTTTGA TGACCCAAAC TCCACTCTCC CTNCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
10	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTNATCT ACAAAGTTTC CAACCGATTT	180
10	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
,	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
15	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
	(2) INFORMATION FOR SEQ ID NO:20:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
25	(ii) MOLECULE TYPE: DNA (genomic)	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
30	GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
30	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
•	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
35	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
40	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATC	333
	(2) INFORMATION FOR SEQ ID NO:21:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
50	(ii) MOLECULE TYPE: DNA (genomic)	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

120

	GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
5	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
10	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCT	300
10	CGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
	(2) INFORMATION FOR SEQ ID NO:22:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: DNA (genomic)	·
•	(xi) SEOUENCE DESCRIPTION: SEO ID NO:22:	
25	GATGTTGTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
	TACCTGCAGA AGCCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
30	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
35	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
•	(2) INFORMATION FOR SEQ ID NO:23:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
50	GATGTTTTGA TGACNCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60

ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG

	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTNATCT ACAAAGTTTC CAACCGATTT	180
	TCTGGGGTCC CAGANAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
5	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
10	(2) INFORMATION FOR SEQ ID NO:24:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 333 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	•
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
20	GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
25	TACCTGCAGA AACCAGGCCN GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
30	AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
30	TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATC	333
	(2) INFORMATION FOR SEQ ID NO:25:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
45	GATGTTTTAA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	60
	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG	120
50	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
50	TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240

		AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG	300
		TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
	5	(2) INFORMATION FOR SEQ ID NO:26:	
	10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	•
		(ii) MOLECULE TYPE: DNA (genomic)	
	15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
		GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC	. 60
	20	ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAGTG GAAACACCTT TTTAGAATGG	120
	20	TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT	180
		TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC	240
	25	AGCAGGGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTAC ACATGTTCCG	300
		TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA	336
	30	(2) INFORMATION FOR SEQ ID NO:27:	•
	-	(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 291 base pairs (B) TYPE: nucleic acid	
	35	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: DNA (genomic)	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	-
	40	CAGGTGCAGC TGCAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
		ACATGCACTG TCTCAGGGTT CTCATTAACC AGCTATGGTA TAACCTGGGT TCGCCAGCCT	120
	45	CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGGTG ACGGAAACAC AAATTATCAT	180
		TCAGCTCTCA TATCCAGACT GAGCATCAGC AAGGATAACT CCAAGAGCCA AGTTTTCTTA	240
	50	AAACTGAACA GTCTGCAAAC TGATGACACA GCCACGTACT ACTGTGCCAA A	291
	50	(2) INFORMATION FOR SEO ID NO:28	

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
	GCTAAGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA	45
	(2) INFORMATION FOR SEQ ID NO:29:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
25	CAGGTGCAGC TGAAGGAGAC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
	ACATGCACCG TCTCAGGGTT CTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT	120
30	CCAGGAAAGG GTCTGGAGTG GCTGGTAGTG ATATGGAGTG ATGGAAGCAC AAACTATAAT	180
50	TCAGCTCTCA AATCCAGACT GAGCATCAGC AAGGACAACT CCAAGAGCCA AGTTTTCTTA	240
	AAAATGAACA GTCTCCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AC	292
35	(2) INFORMATION FOR SEQ ID NO:30:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	·
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
	GGTGACTACT ATGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCA	57
50	(2) INFORMATION FOR SEQ ID NO:31:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs	

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic) ·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
10	CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
10	ACATGCACTG TCTCAGGGTT CTCATTAACC AGCTATGGTG TAAGCTGGGT TCGCCAGCCT	120
	CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGGTG ACGGGAGCAC AAATTATCAT	180
15	TCAGCTCTCA TATCCAGACT GAGCATCAGC AAGGATAACT CCAAGAGCCA AGTTTTCTTA	240
	AAACTGAACA GTCTGCAAAC TGATGACACA GCCACGTACT ACTGTGCCAA GCATCTTGAC	300
20	TACTGGGGCC AAGGCACCAC TCTCACAGTC TCCTCA	336
20	(2) INFORMATION FOR SEQ ID NO:32:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
30	(ii) MOLECULE TYPE: DNA (genomic)(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
	CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
35	ACTTGCACTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT	120
	CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT	180
40	TCGGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA	240
4 0	AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AGGGCATTAC	300
	TACG	304
45	(2) INFORMATION FOR SEQ ID NO:33:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single



	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
5	CTACTATGCT ATGGACTACT GGGGTCAAGG AACCTCAGTC ACCGTCTCC	49
	(2) INFORMATION FOR SEQ ID NO:34:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
20	CAGGTGCAGC TCAAGGAGTC AGGACCTGTC CTCGTGGCGC CCTCACAGAG CCTGTCCATC	60
20	ACTTGCACTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT	120
	CCAGGCAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT	180
25	TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA	240
	AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAA AC	292
30	(2) INFORMATION FOR SEQ ID NO:35:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 50 base pairs (B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
	ACAATGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC NGTCTCCTCA	50
	(2) INFORMATION FOR SEQ ID NO:36:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
- -	(ii) MOLECILE TYPE: DNA (genomic)	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
	CAGGTNCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCAC CCTCACAGAG CCTGTCCATC	60
5	ACATGCÁCTG TCTCTGGGTT CTCATTATCC AGATATAGTG TACACTGGGT TCGCCAGCCT	120
	CCAGGAAAGG GTCTTGAGTG GCTGGGAATG ATATGGGGTG GTGGAAACAC AGACTATAAT	180
10	TCAGCTCTCA AATCCAGACT GAGCATCAGC AAGGACAACT CCAAGAGCCA AGTTTTCTTA	240
10	AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AGATGGTTAC	300
	TACGACTATG CTATGGACTA CTGGGGTCAA GGAACCTCAG TCACCGTCTC C	351
15	(2) INFORMATION FOR SEQ ID NO:37:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
	CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
30	ACTTGCACTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT	120
	CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT	180
	TCGGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA	240
35	AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG A	291
	(2) INFORMATION FOR SEQ ID NO:38:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
50	TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTCC	48
- •	(2) INFORMATION FOR CEO ID NO. 20.	

5	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
10	CACGTGCACC TGAAGGAGTC AGGACCTGTC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
•	ACTTGCACTG TCTCTGGGTT TTCATTAACC AACTATGGTG TACACTGGGT TCGCCAGCCT	120
15	CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAACAC AAATTATAAT	180
	TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAATT CCAAGAGCCA AGTTTTCTTA	240
20	AAAATGAACA GTCTGCAAAT TGATGACACA GCCATATACT ACTGTGCCAA AC	292
	(2) INFORMATION FOR SEQ ID NO:40:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
30	(ii) MOLECULE TYPE: DNA (genomic)(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
	TACTATGCTA TGGACTATTG GGGTCAAGGA ACCTCAGTCA CCGTCTCCTC A	51
35	(2) INFORMATION FOR SEQ ID NO:41:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 288 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
	CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
50	ACTTGCACTG TCTCTGGGTT TCCATTAACC AGCTATGGTG TAGACTGGGT TCGCCAGCCT	120
50	CCAGGAAAGG GTCTGGACTG CCTGGGACTA ATATGGGGTG GTGGAAGGAC NAATTATAAT	180

	TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA	240
	AAAATGAACA GTCTGCNAAC TGATGACACA GCCATGTACT ACTGTGCC	288
5	(2) INFORMATION FOR SEQ ID NO:42:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs	
10	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
	ACGGGGNNTT TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTC	57
	(2) INFORMATION FOR SEQ ID NO:43:	
20	(i) SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 293 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
	CAGGTGCACC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC	60
	ACTTGCACTG TCTCTGGATT TTCATTAACC ACCTATGGTG TACACTGGTT TCGCCAGCCT	120
35	CCAGGAAAGG GTCTGGAGTG GCTGGGACTA ATATGGGCTG GTGGAAACAC AGATTATAAT	180
	TCGGCTCTCA TGTCCAGACT GAGCATCAAC AAAGACAACT CCAAGAGCCA AGTTTTCTTA	240
40	AAAATGAACA GTCTGCAAGC TGATGACACA GCCATGTACT ACTGTGCCAG ATT	293
	(2) INFORMATION FOR SEQ ID NO:44: (i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
JU	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	

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ACGACTATGC TGTGGACTAC TGGGGTCAAG GAACCTCAGT CACCGTCTCC TCA 53 (2) INFORMATION FOR SEQ ID NO:45: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 10 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: 15 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser (2) INFORMATION FOR SEQ ID NO:46: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 25 (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 30 (D) OTHER INFORMATION: /note= "N represents the Nucleotide 30 Inosine(I)" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG 35 35 (2) INFORMATION FOR SEQ ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs 40 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: 45 ACTAGTCGAC ATGGCTGTCY TRGBGCTGYT CYTCTG 36 (2) INFORMATION FOR SEQ ID NO:48: 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
.	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
5	TAATACGACT CACTATAGGG	20
	(2) INFORMATION FOR SEQ ID NO:49:	
10 15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
	GTTTTCCCAG TCACGACGT	19
20	(2) INFORMATION FOR SEQ ID NO:50:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
30	ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCT	39
	(2) INFORMATION FOR SEQ ID NO:51:	
35	(i) SEQUENCÉ CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	,
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
	CCCAAGCTTA CTGGATGGTG GGAAGATGGA	30
45	(2) INFORMATION FOR SEQ ID NO:52:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	

	CAGATGGAAG GGCCCAAC	18
5	(2) INFORMATION FOR SEQ ID NO:53:	
.	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid	٠
10	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	:
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
15	GATTGATGCA TATCATTACC	20
15	(2) INFORMATION FOR SEQ ID NO:54:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	
20	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
23	GTTATCGATG TCGAATAGCC	20
	(2) INFORMATION FOR SEQ ID NO:55:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
	TTGCTGCAGA TTGAGTACTG TTCT	24
40	(2) INFORMATION FOR SEQ ID NO:56:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	,
	(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
50	GCCGATATCA CCATGGCTGT CTTGGGGCTG CTC	33
	(2) INFORMATION FOR SEQ ID NO:57:	-

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5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
10	TTGGGTCATC AAAACATCGG ATCCGCCGCC ACCCGAGCCG CCACCGCCCG AGCCACCTCC	60
	CCCTGAGGAG ACGGTGACTG A	81
15	(2) INFORMATION FOR SEQ ID NO:58:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 81 base pairs(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
٠	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
	TCAGTCACCG TCTCCTCAGG GGGAGGTGGC TCGGGCGGTG GCGGCTCGGG TGGCGGCGGA	60
25	TCCGATGTTT TGATGACCCA A	81
	(2) INFORMATION FOR SEQ ID NO:59:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
	CATCTCTAGA TTATTTGATT TCCAGCTTGG TGCC	34
40	(2) INFORMATION FOR SEQ ID NO:60:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	٠
50	GCCGATATCA CCATGGAGTT GCCTGTTAGG CTG	33
	(2) INFORMATION FOR SEQ ID NO:61:	

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5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
10	TGACTCCTTC ACCTGCACCT GGGATCCGCC GCCACCCGAG CCGCCACCGC CCGAGCCACC	60
	TCCCCCTTTG ATTTCCAGCT TGGTGCC	87
15	(2) INFORMATION FOR SEQ ID NO:62:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	GGCACCAAGC TGGAAATCAA AGGGGGAGGT GGCTCGGGCG GTGGCGGCTC GGGTGGCGGC	60
25	GGATCCCAGG TGCAGGTGAA GGAGTCA	87
	(2) INFORMATION FOR SEQ ID NO:63:	0,
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	CATCTCTAGA TTATGAGGAG ACGGTGACTG AGGT	34
40	(2) INFORMATION FOR SEQ ID NO:64:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
50	ACCATGG	7
	(2) INFORMATION FOR SEQ ID NO:65:	

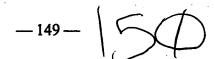
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	5		(i)	(1 (1	A) LI B) T C) S	CE CHENGTHE PROPERTY PER 1 PROPERTY POLICE PROPERTY PROPERTY PROPERTY PER 1 PROPERTY PER 1 PROPERTY PROPERTY PER 1 PROPERTY PROPERTY PROPERTY PER 1 PROPERTY	H: 8: nucl	14 ba leic ESS:	ase p acio doul	pairs i	3							
	10) FE	ATURI A) Ni	LE TY E: AME/I	KEY:	CDS		omic	3)							
	15	GCC	(xi)		CC A	et A	CT G	rc T	IG G	3G C	rg ci	rc T	rc to			al Th		48
	20		CCA Pro			GTC	CTG											96
	25		CTG Leu															144
ij	30		TTC Phe															192
	35.		AAG Lys 195															240
			TAT															288
	40		AAG Lys															336
	45		GCC Ala															384
	50		TGG Trp		Gln												GGC Gly	432
		TCG	GGC	GGT	GGC	GGC	TCG	GGT	GGC	GGC	GGA	TCC	GAT	GTT	TTG	ATG	ACC	480

	Ser	Gly 275	Gly	Gly	Gly	Ser	Gly 280	Gly	Gly	Gly	Ser	Asp 285	Val	Leu	Met	Thr		
5			CCA Pro															528
10			AGA Arg															576
15			TGG Trp		Leu												•	624
15			GTT Val 340															672
20			TCA Ser															720
25			CTG Leu															768
30			GGT Gly									TAAT	CTA	EAG 2	ATG			814
(2) INFORMATION FOR SEQ ID NO:66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear																		
40	(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:																	
45	Met 1	Ala	Val	Leu	Gly 5		Leu	Phe	Сув	Leu 10	Val	Thr	Phe	Pro	Ser 15	Cys		
	Val	Leu	Ser	Gln 20	Val	Gln	Val	Lys	Glu 25	Ser	Gly	Pro	Phe	Leu 30	Val	Pro		
50	Pro	Ser	Gln 35	Ser	Leu	Ser	Ile	Thr 40	Cys	Thr	Val	Ser	Gly 45	Phe	Ser	Leu		
	Thr	Thr	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu		





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5	Glu 65	Trp	Leu	Gly	Ala	Ile 70	Trp	Gly	Asp	Gly	Thr 75	Thr	Asn	Tyr	His	Ser 80
	Ala	Leu	Ile	Ser	Arg 85	Leu	Ser	Ile	Ser	Lys 90	qaA	Asn	Ser	Lys	Ser 95	Gln
10	Val	Phe	Leu	Lys 100	Leu	Asn	Ser	Leu	Gln 105	Thr	Asp	Asp	Thr	Ala 110	Thr	Tyr
	Tyr	Cys	Ala 115	Lys	Leu	Gly	Asn	Tyr 120	Asp	Ala	Leu	Asp	Tyr 125	Trp	Gly	Gln
15	Gly			Val	Thr	Val	Ser 135	Ser	Gly	Gly	Gly	Gly 140	Ser	Gly	Gly	Gly
20	Gly 145	Ser	Gly	Gly	Gly	Gly 150	Ser	Asp	Val	Leu	Met 155	Thr	Gln	Thr	Pro	Leu 160
	Ser	Leu	Pro	Val	Ser 165	Leu	Gly	Asp	Gln	Ala 170	Ser	Ile	Ser	Cys	Arg 175	Ser
25	Ser	Gln	Ser	Ile 180	Val	His	Ser	Asn	Gly 185	Asn	Thr	Tyr	Leu	Glu 190	Trp	Tyr
	Leu	Gln	Lys 195	Pro	Gly	Gln	Ser	Pro 200	Asn	Leu	Leu	Ile	Tyr 205	Phe	Val	Ser
30	Asn	Arg 210	Phe	Ser	Gly	Val	Pro 215	Asp	Arg	Phe	Ser	Gly 220	Ser	Gly	Ser	Gly
25	Thr 225	Asp	Phe	Thr	Leu	Lys 230	Ile	Ser	Arg	Val	Glu 235	Ala	Glu	Asp	Leu	Gly 240
33	Val	Tyr	Tyr	Сув	Phe 245	Gln	Gly	Ser	His	Val 250	Pro	Trp	Thr	Phe	Gly 255	Gly
40	Gly	Thr	Lys	Leu 260	Glu	Ile	Lys									
	1520253035	5 Ala Val 10 Tyr 15 Gly 20 Ser 25 Leu 30 Asn Thr 225 Val Gly	5 Ala Leu Val Phe 10 Tyr Cys 15 Gly Thr 130 Gly Ser 145 20 Ser Leu 25 Leu Gln 30 Asn Arg 210 Thr Asp 225 Val Tyr Gly Thr	Ala Leu Ile Val Phe Leu 10 Tyr Cys Ala 115 Gly Thr Ser 130 Gly Ser Gly 145 Ser Leu Pro Ser Gln Ser Leu Gln Lys 195 30 Asn Arg Phe 210 Thr Asp Phe 225 Val Tyr Tyr Gly Thr Lys	5 Ala Leu Ile Ser Val Phe Leu Lys 100 Tyr Cys Ala Lys 115 15 Gly Thr Ser Val 130 Gly Ser Gly Gly 145 20 Ser Leu Pro Val Ser Gln Ser Ile 180 Leu Gln Lys Pro 195 30 Asn Arg Phe Ser 210 Thr Asp Phe Thr 225 Val Tyr Tyr Cys Gly Thr Lys Leu	Ala Leu Ile Ser Arg 85 Nal Phe Leu Lys Leu 100 Tyr Cys Ala Lys Leu 115 Gly Thr Ser Val Thr 130 Gly Ser Gly Gly Gly 145 Ser Leu Pro Val Ser 165 Ser Gln Ser Ile Val 180 Leu Gln Lys Pro Gly 195 Asn Arg Phe Ser Gly 210 Thr Asp Phe Thr Leu 225 Val Tyr Tyr Cys Phe 245 Gly Thr Lys Leu Glu	5 Ala Leu Ile Ser Arg Leu 85 Nala Leu Ile Ser Arg Leu 85 Val Phe Leu Lys Leu Asn 100 Tyr Cys Ala Lys Leu Gly 115 Gly Thr Ser Val Thr Val 130 Gly Ser Gly Gly Gly Gly Gly 145 Ser Leu Pro Val Ser Leu 165 Ser Gln Ser Ile Val His 180 Leu Gln Lys Pro Gly Gln 195 Leu Gln Lys Pro Gly Gln 195 Asn Arg Phe Ser Gly Val 210 Thr Asp Phe Thr Leu Lys 230 Val Tyr Tyr Cys Phe Gln 245	5 Ala Leu Ile Ser Arg Leu Ser 10 Val Phe Leu Lys Leu Asn Ser 10 Tyr Cys Ala Lys Leu Gly Asn 115 Gly Thr Ser Val Thr Val Ser 130 Ser Gly Gly Gly Gly Ser 145 Ser Gly Gly Gly Gly Ser 145 Ser Ile Val His Ser 20 Ser Leu Pro Val Ser Leu Gly 165 Leu Gln Lys Pro Gly Gln Ser 195 Thr Asp Phe Ser Gly Val Pro 215 Thr Asp Phe Thr Leu Lys Ile 225 Val Tyr Tyr Cys Phe Gln Gly 245 Gly Thr Lys Leu Glu Ile Lys	5 Ala Leu Ile Ser Arg Leu Ser Ile 85 10 Val Phe Leu Lys Leu Asn Ser Leu 100 Tyr Cys Ala Lys Leu Gly Asn Tyr 120 15 Gly Thr Ser Val Thr Val Ser Ser 135 Gly Ser Gly Gly Gly Gly Ser Asp 150 Ser Leu Pro Val Ser Leu Gly Asp 150 Ser Gln Ser Ile Val His Ser Asn 180 Leu Gln Lys Pro Gly Gln Ser Pro 195 Leu Gln Lys Pro Gly Gln Ser Pro 200 30 Asn Arg Phe Ser Gly Val Pro Asp 215 Thr Asp Phe Thr Leu Lys Ile Ser 235 Val Tyr Tyr Cys Phe Gln Gly Ser 35 Val Tyr Tyr Cys Phe Gln Gly Ser 35 Gly Thr Lys Leu Glu Ile Lys	5 Ala Leu Ile Ser Arg Leu Ser Ile Ser 85	Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys 90 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr 100 105 Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala 115 Gly Thr Ser Val Thr Val Ser Ser Gly Gly 135 Gly Ser Gly Gly Gly Gly Ser Asp Val Leu 145 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala 165 Ser Gln Ser Ile Val His Ser Asn Gly Asn 185 Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu 195 Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu 195 Thr Asp Phe Thr Leu Lys Ile Ser Arg Val 220 Thr Asp Phe Thr Leu Lys Ile Ser Arg Val 225 Val Tyr Tyr Cys Phe Gln Gly Ser His Val 245 Gly Thr Lys Leu Glu Ile Lys	5 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp 90 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp 100 Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu 115 Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly 130 Gly Ser Gly Gly Gly Gly Ser Asp Val Leu Met 145 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser 170 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser 170 Ser Gln Ser Ile Val His Ser Asp Gly Asp Thr 185 Leu Gln Lys Pro Gly Gln Ser Pro Asp Leu Leu 200 30 Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser 215 Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu 235 Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro 245 Gly Thr Lys Leu Glu Ile Lys	5 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn 85	5 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser 85	5 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys 85 Leu 100	Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser 95 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr 100 Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly 125 Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly 130 Gly Ser Gly Gly Gly Gly Ser Asp Val Leu Met Thr Gln Thr Pro 145 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg 170 Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp 180 Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val 195 Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Ser Cys Arg 215 Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly 255 Gly Thr Lys Leu Glu Ile Lys